

SEQUENCE LISTING

<110> Dartois, Veronique A.
Hoch, James A.
Valle, Fernando
Kumar, Manoj

<120> 2,5-DKG Permeases

<130> GC687-3-D1

<140> US 10/787,267

<141> 2004-02-25

<150> US 09/922,501

<151> 2001-08-03

<150> US 60/325,774

<151> 2000-08-04

<150> US 60/421,141

<151> 2000-09-29

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<221> CDS

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Met Asn Ser Ser Thr Asn Ala
1 5

acg aaa cgc tgg tgg tac atc atg cct atc gtg ttt atc acg tat agc 162
Thr Lys Arg Trp Trp Tyr Ile Met Pro Ile Val Phe Ile Thr Tyr Ser
10 15 20

ctg gcg tat ctc gac cgc gca aac ttc agc ttt gct tcg gca gcg ggc 210
Leu Ala Tyr Leu Asp Arg Ala Asn Phe Ser Phe Ala Ser Ala Ala Gly
25 30 35

att acg gaa gat tta ggc att acc aaa ggc atc tcg tcg ctt ctt ggc 258
Ile Thr Glu Asp Leu Gly Ile Thr Lys Gly Ile Ser Ser Leu Leu Gly
40 45 50 55

gca ctt ttc ttc ctc ggc tat ttc ttc ttc cag atc ccg ggg gcg att 306



Ala Leu Phe Phe Leu Gly Tyr Phe Phe Phe Gln Ile Pro Gly Ala Ile	
60 65 70	
tac gcg gaa cgc cgt agc gta cgg aag ctg att ttc atc tgt ctg atc	354
Tyr Ala Glu Arg Arg Ser Val Arg Lys Leu Ile Phe Ile Cys Leu Ile	
75 80 85	
ctg tgg ggc gcc tgc gcc tcg ctt gac cgg gat ggt gca caa tat tcc	402
Leu Trp Gly Ala Cys Ala Ser Leu Asp Arg Asp Gly Ala Gln Tyr Ser	
90 95 100	
agc gct ggc tgg cga tcc gtt tta ttc tcg gct gtc gtg gaa gcg gcg	450
Ser Ala Gly Trp Arg Ser Val Leu Phe Ser Ala Val Val Glu Ala Ala	
105 110 115	
gtc atg ccg gcg atg ctg att tac atc agt aac tgg ttt acc aaa tca	498
Val Met Pro Ala Met Leu Ile Tyr Ile Ser Asn Trp Phe Thr Lys Ser	
120 125 130 135	
gaa cgt tca cgc gcc aac acc ttc tta atc ctc ggc aac ccg gtc acg	546
Glu Arg Ser Arg Ala Asn Thr Phe Leu Ile Leu Gly Asn Pro Val Thr	
140 145 150	
gta ctg tgg atg tcg gtg gtc tcc ggc tac ctg att cag tcc ttc ggc	594
Val Leu Trp Met Ser Val Val Ser Gly Tyr Leu Ile Gln Ser Phe Gly	
155 160 165	
tgg cgt gaa atg ttt att att gaa ggc gtt ccg gcc gtc ctc tgg gcc	642
Trp Arg Glu Met Phe Ile Ile Glu Gly Val Pro Ala Val Leu Trp Ala	
170 175 180	
ttc tgc tgg tgg gtg ctg gtc aaa gtt aaa ccg tcg cag gtg aac tgg	690
Phe Cys Trp Trp Val Leu Val Lys Val Lys Pro Ser Gln Val Asn Trp	
185 190 195	
ttg tcg gaa aac gag aaa gcc gcg ctg cag gcg cag ctg gag agc gag	738
Leu Ser Glu Asn Glu Lys Ala Ala Leu Gln Ala Gln Leu Glu Ser Glu	
200 205 210 215	
cag cag ggt att aaa gcc gtg cgt aac tac ggc gaa gcc ttc cgc tca	786
Gln Gln Gly Ile Lys Ala Val Arg Asn Tyr Gly Glu Ala Phe Arg Ser	
220 225 230	
cgc aac gtc att cta ctg tgc atg cag tat ttt gcc tgg agt atc ggc	834
Arg Asn Val Ile Leu Leu Cys Met Gln Tyr Phe Ala Trp Ser Ile Gly	
235 240 245	
gtg tac ggt ttt gtg ctg tgg ttg ccg tca att att cgc agc ggc ggc	882
Val Tyr Gly Phe Val Leu Trp Leu Pro Ser Ile Ile Arg Ser Gly Gly	
250 255 260	
gtc aat atg ggg atg gtg gaa gtc ggc tgg ctc tct tcg gtg cct tat	930
Val Asn Met Gly Met Val Glu Val Gly Trp Leu Ser Ser Val Pro Tyr	
265 270 275	
ctg gcc gcg act att gcg atg atc gtc gtc tcc tgg gct tcc gat aaa	978
Leu Ala Ala Thr Ile Ala Met Ile Val Val Ser Trp Ala Ser Asp Lys	

280	285	290	295	
atg cag aac cgt aaa ctg ttc gtc tgg ccg ctg ctg ctg att ggc gga				1026
Met Gln Asn Arg Lys Leu Phe Val Trp Pro Leu Leu Leu Ile Gly Gly				
300		305	310	
ctg gct ttt att ggc tca tgg gcc gtc ggc gct aac cat ttc tgg gcc				1074
Leu Ala Phe Ile Gly Ser Trp Ala Val Gly Ala Asn His Phe Trp Ala				
315		320	325	
tct tat acc ctg ctg gtg att gcc aat gcg gca atg tac gcc cct tac				1122
Ser Tyr Thr Leu Leu Val Ile Ala Asn Ala Ala Met Tyr Ala Pro Tyr				
330		335	340	
ggc ccg ttt ttc gcc atc att ccg gaa atg ctg ccg cgt aac gtc gcc				1170
Gly Pro Phe Phe Ala Ile Ile Pro Glu Met Leu Pro Arg Asn Val Ala				
345		350	355	
ggc ggc gca atg gcg ctc atc aac agc atg ggc gcc tta ggt tca ttc				1218
Gly Gly Ala Met Ala Leu Ile Asn Ser Met Gly Ala Leu Gly Ser Phe				
360		365	370	375
ttt ggt tcg tgg ttc gtg ggc tac ctg aac ggc acc acc ggc agt cca				1266
Phe Gly Ser Trp Phe Val Gly Tyr Leu Asn Gly Thr Thr Gly Ser Pro				
380		385	390	
tca gcc tca tac att ttc atg gga gtg gcg ctt ttc gcc tcg gta tgg				1314
Ser Ala Ser Tyr Ile Phe Met Gly Val Ala Leu Phe Ala Ser Val Trp				
395		400	405	
ctt act tta att gtt aag cct gct aac aat caa aag ctc ccc atc ggc				1362
Leu Thr Leu Ile Val Lys Pro Ala Asn Asn Gln Lys Leu Pro Ile Gly				
410		415	420	
gct cgt cac gcc tgacctttac tacttacgga gatcacgcct tgggtacgtt				1414
Ala Arg His Ala				
425				
gcaggacaaa ccgataggca ccgcaaaggc tggggccatc gagcagcgcg taaacagtca				1474
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<212> PRT

<213> environmental source

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Ser Phe Ala Ser Ala Ala Gly Ile Thr Glu Asp Leu Gly Ile Thr Lys				
35	40	45		
Gly Ile Ser Ser Leu Leu Gly Ala Leu Phe Phe Leu Gly Tyr Phe Phe				
50	55	60		
Phe Gln Ile Pro Gly Ala Ile Tyr Ala Glu Arg Arg Ser Val Arg Lys				
65	70	75	80	

Leu Ile Phe Ile Cys Leu Ile Leu Trp Gly Ala Cys Ala Ser Leu Asp
 85 90 95
 Arg Asp Gly Ala Gln Tyr Ser Ser Ala Gly Trp Arg Ser Val Leu Phe
 100 105 110
 Ser Ala Val Val Glu Ala Ala Val Met Pro Ala Met Leu Ile Tyr Ile
 115 120 125
 Ser Asn Trp Phe Thr Lys Ser Glu Arg Ser Arg Ala Asn Thr Phe Leu
 130 135 140
 Ile Leu Gly Asn Pro Val Thr Val Leu Trp Met Ser Val Val Ser Gly
 145 150 155 160
 Tyr Leu Ile Gln Ser Phe Gly Trp Arg Glu Met Phe Ile Ile Glu Gly
 165 170 175
 Val Pro Ala Val Leu Trp Ala Phe Cys Trp Trp Val Leu Val Lys Val
 180 185 190
 Lys Pro Ser Gln Val Asn Trp Leu Ser Glu Asn Glu Lys Ala Ala Leu
 195 200 205
 Gln Ala Gln Leu Glu Ser Glu Gln Gln Gly Ile Lys Ala Val Arg Asn
 210 215 220
 Tyr Gly Glu Ala Phe Arg Ser Arg Asn Val Ile Leu Leu Cys Met Gln
 225 230 235 240
 Tyr Phe Ala Trp Ser Ile Gly Val Tyr Gly Phe Val Leu Trp Leu Pro
 245 250 255
 Ser Ile Ile Arg Ser Gly Gly Val Asn Met Gly Met Val Glu Val Gly
 260 265 270
 Trp Leu Ser Ser Val Pro Tyr Leu Ala Ala Thr Ile Ala Met Ile Val
 275 280 285
 Val Ser Trp Ala Ser Asp Lys Met Gln Asn Arg Lys Leu Phe Val Trp
 290 295 300
 Pro Leu Leu Leu Ile Gly Gly Leu Ala Phe Ile Gly Ser Trp Ala Val
 305 310 315 320
 Gly Ala Asn His Phe Trp Ala Ser Tyr Thr Leu Leu Val Ile Ala Asn
 325 330 335
 Ala Ala Met Tyr Ala Pro Tyr Gly Pro Phe Phe Ala Ile Ile Pro Glu
 340 345 350
 Met Leu Pro Arg Asn Val Ala Gly Gly Ala Met Ala Leu Ile Asn Ser
 355 360 365
 Met Gly Ala Leu Gly Ser Phe Phe Gly Ser Trp Phe Val Gly Tyr Leu
 370 375 380
 Asn Gly Thr Thr Gly Ser Pro Ser Ala Ser Tyr Ile Phe Met Gly Val
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<222> (214)...(1491)

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aacaccgagt ttataaccct gaacgacacg gctgcgggcc tgtgtagacg cccctacgcc	180
ttaacaccac taaatgactc tacaggtgta tat atg aat aca gcc tct gtt tct	234
Met Asn Thr Ala Ser Val Ser	
1 5	
gtc acc caa agc cag gcg atc ccc aaa tta cgc tgg ttg aga ata gtg	282
Val Thr Gln Ser Gln Ala Ile Pro Lys Leu Arg Trp Leu Arg Ile Val	
10 15 20	
ccg cct att ctt att acc tgc att att tcc tat atg gac cgg gtg aac	330
Pro Pro Ile Leu Ile Thr Cys Ile Ile Ser Tyr Met Asp Arg Val Asn	
25 30 35	
atc gcc ttc gcc atg ccc ggc ggc atg gac gat gaa ctg ggc atc acc	378
Ile Ala Phe Ala Met Pro Gly Gly Met Asp Asp Glu Leu Gly Ile Thr	
40 45 50 55	
gcc tcg atg gcc ggg ttg gcc ggc ggt att ttc ttt atc ggt tat ctg	426
Ala Ser Met Ala Gly Leu Ala Gly Gly Ile Phe Phe Ile Gly Tyr Leu	
60 65 70	
ttc ttg cag gta ccc ggc ggc aag ctg gcg gtg tac ggc aac ggc aag	474
Phe Leu Gln Val Pro Gly Gly Lys Leu Ala Val Tyr Gly Asn Gly Lys	
75 80 85	
aaa ttc atc ggt tgg tcg ttg ttg gcc tgg gcg gtg att tcc gtg ctg	522
Lys Phe Ile Gly Trp Ser Leu Leu Ala Trp Ala Val Ile Ser Val Leu	
90 95 100	
acc ggg ctg gtc acg aat cag tat caa ttg ctg ttc ctg cgc ttc gcc	570
Thr Gly Leu Val Thr Asn Gln Tyr Gln Leu Leu Phe Leu Arg Phe Ala	
105 110 115	
ctc ggc cgt ttc cga agc ggc atg ctg cgg tgg gtg ctg acc atg atc	618
Leu Gly Arg Phe Arg Ser Gly Met Leu Arg Trp Val Leu Thr Met Ile	
120 125 130 135	
agc aac tgg ttc ccg gac aag gaa cgc ggg cgc gcc aac gcc atc gtc	666
Ser Asn Trp Phe Pro Asp Lys Glu Arg Gly Arg Ala Asn Ala Ile Val	
140 145 150	
atc atg ttc gtg ccg atc gcc ggc atc ctt acc gca ccg ctg tcc ggc	714
Ile Met Phe Val Pro Ile Ala Gly Ile Leu Thr Ala Pro Leu Ser Gly	
155 160 165	
tgg atc atc acc gcc tgg gac tgg cgc atg ctg ttc ctg gtc gag ggc	762
Trp Ile Ile Thr Ala Trp Asp Trp Arg Met Leu Phe Leu Val Glu Gly	
170 175 180	
gcg ctg tcg ctg gtc gtg atg gtg ctg tgg tat ttc acc atc agc aac	810
Ala Leu Ser Leu Val Val Met Val Leu Trp Tyr Phe Thr Ile Ser Asn	
185 190 195	
cgt cca caa gag gcc aaa agg att tcg cag gcg gaa aaa gat tat ctg	858
Arg Pro Gln Glu Ala Lys Arg Ile Ser Gln Ala Glu Lys Asp Tyr Leu	
200 205 210 215	

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cgc aac gcc tcg ctg cgt cgg gtg ctg ggc gac aaa atc atg tgg aag Arg Asn Ala Ser Leu Arg Arg Val Leu Gly Asp Lys Ile Met Trp Lys 235 240 245	954
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att ctc aag ggg ctc acc aac ggc aat atg gag cag gtc ggg atg ctg Ile Leu Lys Gly Leu Thr Asn Gly Asn Met Glu Gln Val Gly Met Leu 265 270 275	1050
gct atc ctg ccc tat atc ggc gcc atc ttc ggc atg ctg atc att tcc Ala Ile Leu Pro Tyr Ile Gly Ala Ile Phe Gly Met Leu Ile Ile Ser 280 285 290 295	1098
acc ctc tcc gat cgc acc ggc aag cgc aaa gtg ttc gtc gca ctg ccg Thr Leu Ser Asp Arg Thr Gly Lys Arg Lys Val Phe Val Ala Leu Pro 300 305 310	1146
ctg gcc tgc ttt gcc atc tgc atg gcg ctg tcg gtg ctg ctg aag gat Leu Ala Cys Phe Ala Ile Cys Met Ala Leu Ser Val Leu Leu Lys Asp 315 320 325	1194
cac atc tgg tgg tcg tac gcg gcg ctg gtg ggc tgt ggc gtc ttt acc His Ile Trp Trp Ser Tyr Ala Ala Leu Val Gly Cys Gly Val Phe Thr 330 335 340	1242
cag gcc gcc gcc ggg gtg ttc tgg acc att ccg ccc aag ctg ttt aac Gln Ala Ala Ala Gly Val Phe Trp Thr Ile Pro Pro Lys Leu Phe Asn 345 350 355	1290
gcc gaa atg gcc ggc ggc gcg cgc ggc gtg atc aat gca ctg ggc aac Ala Glu Met Ala Gly Gly Ala Arg Gly Val Ile Asn Ala Leu Gly Asn 360 365 370 375	1338
ctc ggc ggt ttc tgc ggc ccc tat atg gtc ggc gtg ttg atc acc ttg Leu Gly Gly Phe Cys Gly Pro Tyr Met Val Gly Val Leu Ile Thr Leu 380 385 390	1386
ttc agc aaa gac gtc ggc gtt tac agc ctc gcg gtg tcg ctg gcc tcc Phe Ser Lys Asp Val Gly Val Tyr Ser Leu Ala Val Ser Leu Ala Ser 395 400 405	1434
gcc tcg gtg ctg gcg ttg atg ctg ccg aac aga tgc gac caa aaa gcg Ala Ser Val Leu Ala Leu Met Leu Pro Asn Arg Cys Asp Gln Lys Ala 410 415 420	1482
ggg gcc gaa taatggacta ttggctgggg ctggactgcg gcggcacctt Gly Ala Glu 425	1531
tatcaaagcc ggctgtatg accggaatgg cgcagaactg ggcatagccc gccgtacgct	1591

ggacattgtc	gcgcccgaac	ccggctgggc	ggaacgtgac	atgcccgcgc	tgtggcagac	1651
cgccgcgcgag	gtgatccgcg	aattgctggc	ccgcaacgac	attgccgacg	ctgatattca	1711
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gttg						1775

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			20					25					30		
Ser	Tyr	Met	Asp	Arg	Val	Asn	Ile	Ala	Phe	Ala	Met	Pro	Gly	Gly	Met
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Asp	Asp	Glu	Leu	Gly	Ile	Thr	Ala	Ser	Met	Ala	Gly	Leu	Ala	Gly	Gly
	50					55					60				
Ile	Phe	Phe	Ile	Gly	Tyr	Leu	Phe	Leu	Gln	Val	Pro	Gly	Gly	Lys	Leu
65					70				75						80
Ala	Val	Tyr	Gly	Asn	Gly	Lys	Lys	Phe	Ile	Gly	Trp	Ser	Leu	Leu	Ala
				85					90					95	
Trp	Ala	Val	Ile	Ser	Val	Leu	Thr	Gly	Leu	Val	Thr	Asn	Gln	Tyr	Gln
			100					105					110		
Leu	Leu	Phe	Leu	Arg	Phe	Ala	Leu	Gly	Arg	Phe	Arg	Ser	Gly	Met	Leu
		115					120					125			
Arg	Trp	Val	Leu	Thr	Met	Ile	Ser	Asn	Trp	Phe	Pro	Asp	Lys	Glu	Arg
	130					135					140				
Gly	Arg	Ala	Asn	Ala	Ile	Val	Ile	Met	Phe	Val	Pro	Ile	Ala	Gly	Ile
145					150					155					160
Leu	Thr	Ala	Pro	Leu	Ser	Gly	Trp	Ile	Ile	Thr	Ala	Trp	Asp	Trp	Arg
				165					170					175	
Met	Leu	Phe	Leu	Val	Glu	Gly	Ala	Leu	Ser	Leu	Val	Val	Met	Val	Leu
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Trp	Tyr	Phe	Thr	Ile	Ser	Asn	Arg	Pro	Gln	Glu	Ala	Lys	Arg	Ile	Ser
		195					200					205			
Gln	Ala	Glu	Lys	Asp	Tyr	Leu	Ile	Lys	Thr	Leu	His	Asp	Glu	Gln	Leu
	210					215					220				
Leu	Ile	Lys	Gly	Lys	Thr	Val	Arg	Asn	Ala	Ser	Leu	Arg	Arg	Val	Leu
225					230					235					240
Gly	Asp	Lys	Ile	Met	Trp	Lys	Phe	Phe	Tyr	Gln	Thr	Gly	Ile	Tyr	Gly
			245						250					255	
Tyr	Thr	Leu	Trp	Leu	Pro	Thr	Ile	Leu	Lys	Gly	Leu	Thr	Asn	Gly	Asn
		260						265					270		
Met	Glu	Gln	Val	Gly	Met	Leu	Ala	Ile	Leu	Pro	Tyr	Ile	Gly	Ala	Ile
		275					280					285			
Phe	Gly	Met	Leu	Ile	Ile	Ser	Thr	Leu	Ser	Asp	Arg	Thr	Gly	Lys	Arg
	290					295					300				
Lys	Val	Phe	Val	Ala	Leu	Pro	Leu	Ala	Cys	Phe	Ala	Ile	Cys	Met	Ala
305					310					315					320
Leu	Ser	Val	Leu	Leu	Lys	Asp	His	Ile	Trp	Trp	Ser	Tyr	Ala	Ala	Leu
				325					330					335	
Val	Gly	Cys	Gly	Val	Phe	Thr	Gln	Ala	Ala	Ala	Gly	Val	Phe	Trp	Thr
			340					345					350		
Ile	Pro	Pro	Lys	Leu	Phe	Asn	Ala	Glu	Met	Ala	Gly	Gly	Ala	Arg	Gly
		355					360						365		

Val Ile Asn Ala Leu Gly Asn Leu Gly Gly Phe Cys Gly Pro Tyr Met
 370 375 380
 Val Gly Val Leu Ile Thr Leu Phe Ser Lys Asp Val Gly Val Tyr Ser
 385 390 395 400
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 Asn Arg Cys Asp Gln Lys Ala Gly Ala Glu
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<210> 5
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 <212> DNA
 <213> Klebsiella oxytoca

<220>
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 Met Asn Ser Ser Thr Asn Ala Thr Lys Arg Trp Trp Tyr
 1 5 10
 atc atg cct atc gtg ttt atc acg tat agc ctg gcg tac ctc gac cgc 159
 Ile Met Pro Ile Val Phe Ile Thr Tyr Ser Leu Ala Tyr Leu Asp Arg
 15 20 25
 gct aac ttc agc ttc gct tcg gcg gcc gga att act gaa gac ctg ggg 207
 Ala Asn Phe Ser Phe Ala Ser Ala Ala Gly Ile Thr Glu Asp Leu Gly
 30 35 40 45
 atc acc aaa ggt atc tcc tcc ctt ctg ggg gcg ctg ttc ttc ctc ggc 255
 Ile Thr Lys Gly Ile Ser Ser Leu Leu Gly Ala Leu Phe Phe Leu Gly
 50 55 60
 tac ttc ttc ttt cag atc ccc ggc gcg att tat gcc gaa cgc cgc agc 303
 Tyr Phe Phe Phe Gln Ile Pro Gly Ala Ile Tyr Ala Glu Arg Arg Ser
 65 70 75
 gta cgt aaa ctc att ttc atc tgc ctg atc ctg tgg ggt gcc tgc gcc 351
 Val Arg Lys Leu Ile Phe Ile Cys Leu Ile Leu Trp Gly Ala Cys Ala
 80 85 90
 tca ctc gac cgg gat ggt gca caa tat tcc cgc gct ggg cgg gcg atc 399
 Ser Leu Asp Arg Asp Gly Ala Gln Tyr Ser Arg Ala Gly Arg Ala Ile
 95 100 105
 cgc ttt atc ctt ggc gtg gtc gag gcc gca gtc atg ccg gcg atg ctg 447
 Arg Phe Ile Leu Gly Val Val Glu Ala Ala Val Met Pro Ala Met Leu
 110 115 120 125
 ata tac atc agc aac tgg ttt acc aaa tcc gaa cgc tcg cgc gcc aat 495
 Ile Tyr Ile Ser Asn Trp Phe Thr Lys Ser Glu Arg Ser Arg Ala Asn
 130 135 140
 acc ttc ctg atc ctc ggc aac ccg gtg acg gtg ctg tgg atg tcg gtg 543

Thr	Phe	Leu	Ile	Leu	Gly	Asn	Pro	Val	Thr	Val	Leu	Trp	Met	Ser	Val		
			145					150					155				
gtc	tcc	ggc	tac	ctg	att	cag	gct	ttc	ggc	tgg	cgg	gag	atg	ttt	att		591
Val	Ser	Gly	Tyr	Leu	Ile	Gln	Ala	Phe	Gly	Trp	Arg	Glu	Met	Phe	Ile		
		160					165					170					
att	gaa	ggc	gtt	ccg	gcg	gtg	att	tgg	gcc	ttc	tgc	tgg	tgg	gtg	ctg		639
Ile	Glu	Gly	Val	Pro	Ala	Val	Ile	Trp	Ala	Phe	Cys	Trp	Trp	Val	Leu		
	175					180					185						
gta	aaa	gat	aaa	ccg	tct	cag	gtc	aac	tgg	ctg	gcg	gaa	agc	gaa	aag		687
Val	Lys	Asp	Lys	Pro	Ser	Gln	Val	Asn	Trp	Leu	Ala	Glu	Ser	Glu	Lys		
190					195				200						205		
gcc	gca	ttg	cag	gag	cag	ctg	gag	cgc	gaa	cag	cag	ggc	atc	aaa	ccg		735
Ala	Ala	Leu	Gln	Glu	Gln	Leu	Glu	Arg	Glu	Gln	Gln	Gly	Ile	Lys	Pro		
			210					215						220			
gtg	cgc	aac	tac	ggc	gag	gcc	ttc	cgc	tgc	cgt	aac	gtg	gtc	ctg	ctg		783
Val	Arg	Asn	Tyr	Gly	Glu	Ala	Phe	Arg	Ser	Arg	Asn	Val	Val	Leu	Leu		
		225					230					235					
tgc	atg	caa	tat	ttc	gcc	tgg	agc	atc	ggg	gtt	tac	ggc	ttc	gtg	ctg		831
Cys	Met	Gln	Tyr	Phe	Ala	Trp	Ser	Ile	Gly	Val	Tyr	Gly	Phe	Val	Leu		
	240					245					250						
tgg	ctg	ccg	tca	att	atc	cgc	agc	ggc	ggc	gag	aat	atg	ggc	atg	gtc		879
Trp	Leu	Pro	Ser	Ile	Ile	Arg	Ser	Gly	Gly	Glu	Asn	Met	Gly	Met	Val		
	255					260					265						
gag	gtc	ggc	tgg	ctc	tca	tcc	gtc	ccc	tac	ctg	gcg	gca	acc	atc	gcc		927
Glu	Val	Gly	Trp	Leu	Ser	Ser	Val	Pro	Tyr	Leu	Ala	Ala	Thr	Ile	Ala		
270				275					280						285		
atg	atc	gtg	gtc	tcc	tgg	gcc	tcc	gat	aaa	atg	cag	aac	cgc	aag	cta		975
Met	Ile	Val	Val	Ser	Trp	Ala	Ser	Asp	Lys	Met	Gln	Asn	Arg	Lys	Leu		
			290					295					300				
ttc	gtc	tgg	ccg	ctg	ctg	ctg	att	gcc	gcc	ttc	gcg	ttt	att	ggc	tcc		1023
Phe	Val	Trp	Pro	Leu	Leu	Leu	Ile	Ala	Ala	Phe	Ala	Phe	Ile	Gly	Ser		
			305				310						315				
tgg	gcc	gtc	ggc	gct	aac	cat	ttc	tgg	gtc	tct	tat	acc	ctg	ctg	gtc		1071
Trp	Ala	Val	Gly	Ala	Asn	His	Phe	Trp	Val	Ser	Tyr	Thr	Leu	Leu	Val		
	320					325					330						
att	gcc	ggc	gcg	gcg	atg	tac	gcc	ccc	tac	ggg	ccg	ttc	ttc	gcc	atc		1119
Ile	Ala	Gly	Ala	Ala	Met	Tyr	Ala	Pro	Tyr	Gly	Pro	Phe	Phe	Ala	Ile		
	335				340					345							
att	ccc	gag	atg	ctg	ccg	cgt	aac	gtc	gcc	ggg	ggc	gcc	atg	gcg	ctg		1167
Ile	Pro	Glu	Met	Leu	Pro	Arg	Asn	Val	Ala	Gly	Gly	Ala	Met	Ala	Leu		
350				355				360						365			
att	aac	agc	atg	ggc	gcg	ctg	ggc	tca	ttc	ttt	ggc	tca	tgg	ttt	gtc		1215
Ile	Asn	Ser	Met	Gly	Ala	Leu	Gly	Ser	Phe	Phe	Gly	Ser	Trp	Phe	Val		

370	375	380	
ggc tac ctg aac ggc acc acc ggc agc ccg tca gcc tcg tac att ttt			1263
Gly Tyr Leu Asn Gly Thr Thr Gly Ser Pro Ser Ala Ser Tyr Ile Phe			
385	390	395	
atg gga gtg gcg ctt ttc gtc tcg gta tgg ctt act ttg att gtt aag			1311
Met Gly Val Ala Leu Phe Val Ser Val Trp Leu Thr Leu Ile Val Lys			
400	405	410	
cct gct aat aat caa aaa ctt ccg ctc ggc gca cgt cac gcc			1353
Pro Ala Asn Asn Gln Lys Leu Pro Leu Gly Ala Arg His Ala			
415	420	425	
tgaacatta acgcaacgga gaaccgcatg aagccgtcag tcattctcta caaaacgctt			1413
cccgacgacc tgcaacaagc gtctggaaca acactttacc gtcacgcagg tgaaaaacct			1473
gcgtt			1478
<210> 6			
<211> 427			
<212> PRT			
<213> Klebsiella oxytoca			
<400> 6			
Met Asn Ser Ser Thr Asn Ala Thr Lys Arg Trp Trp Tyr Ile Met Pro			
1	5	10	15
Ile Val Phe Ile Thr Tyr Ser Leu Ala Tyr Leu Asp Arg Ala Asn Phe			
20	25	30	
Ser Phe Ala Ser Ala Ala Gly Ile Thr Glu Asp Leu Gly Ile Thr Lys			
35	40	45	
Gly Ile Ser Ser Leu Leu Gly Ala Leu Phe Phe Leu Gly Tyr Phe Phe			
50	55	60	
Phe Gln Ile Pro Gly Ala Ile Tyr Ala Glu Arg Arg Ser Val Arg Lys			
65	70	75	80
Leu Ile Phe Ile Cys Leu Ile Leu Trp Gly Ala Cys Ala Ser Leu Asp			
85	90	95	
Arg Asp Gly Ala Gln Tyr Ser Arg Ala Gly Arg Ala Ile Arg Phe Ile			
100	105	110	
Leu Gly Val Val Glu Ala Ala Val Met Pro Ala Met Leu Ile Tyr Ile			
115	120	125	
Ser Asn Trp Phe Thr Lys Ser Glu Arg Ser Arg Ala Asn Thr Phe Leu			
130	135	140	
Ile Leu Gly Asn Pro Val Thr Val Leu Trp Met Ser Val Val Ser Gly			
145	150	155	160
Tyr Leu Ile Gln Ala Phe Gly Trp Arg Glu Met Phe Ile Ile Glu Gly			
165	170	175	
Val Pro Ala Val Ile Trp Ala Phe Cys Trp Trp Val Leu Val Lys Asp			
180	185	190	
Lys Pro Ser Gln Val Asn Trp Leu Ala Glu Ser Glu Lys Ala Ala Leu			
195	200	205	
Gln Glu Gln Leu Glu Arg Glu Gln Gln Gly Ile Lys Pro Val Arg Asn			
210	215	220	
Tyr Gly Glu Ala Phe Arg Ser Arg Asn Val Val Leu Leu Cys Met Gln			
225	230	235	240
Tyr Phe Ala Trp Ser Ile Gly Val Tyr Gly Phe Val Leu Trp Leu Pro			
245	250	255	
Ser Ile Ile Arg Ser Gly Gly Glu Asn Met Gly Met Val Glu Val Gly			

260 265 270
 Trp Leu Ser Ser Val Pro Tyr Leu Ala Ala Thr Ile Ala Met Ile Val
 275 280 285
 Val Ser Trp Ala Ser Asp Lys Met Gln Asn Arg Lys Leu Phe Val Trp
 290 295 300
 Pro Leu Leu Leu Ile Ala Ala Phe Ala Phe Ile Gly Ser Trp Ala Val
 305 310 315 320
 Gly Ala Asn His Phe Trp Val Ser Tyr Thr Leu Leu Val Ile Ala Gly
 325 330 335
 Ala Ala Met Tyr Ala Pro Tyr Gly Pro Phe Phe Ala Ile Ile Pro Glu
 340 345 350
 Met Leu Pro Arg Asn Val Ala Gly Gly Ala Met Ala Leu Ile Asn Ser
 355 360 365
 Met Gly Ala Leu Gly Ser Phe Phe Gly Ser Trp Phe Val Gly Tyr Leu
 370 375 380
 Asn Gly Thr Thr Gly Ser Pro Ser Ala Ser Tyr Ile Phe Met Gly Val
 385 390 395 400
 Ala Leu Phe Val Ser Val Trp Leu Thr Leu Ile Val Lys Pro Ala Asn
 405 410 415
 Asn Gln Lys Leu Pro Leu Gly Ala Arg His Ala
 420 425

<210> 7
 <211> 1600
 <212> DNA
 <213> Pantoea citrea

<220>
 <221> CDS
 <222> (214)...(1521)

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 acactttctt aacatgccct tacgtgaccc tgatcccaca ctgtcagtgcc aaaaacacgt 120
 tttatagctc ctgataagca cagttcgcag cgcgtaactg caccgcgagg gttctgcttt 180
 gcgtcaactg acaaaacaga aaggggatat atc atg caa aaa tca cag ccg gga 234
 Met Gln Lys Ser Gln Pro Gly
 1 5
 acc cgc tgg ttt cgg att att gtg ccg atc ctg ata gcc tgc atc atg 282
 Thr Arg Trp Phe Arg Ile Ile Val Pro Ile Leu Ile Ala Cys Ile Met
 10 15 20
 tcg ttt atg gat cgg gta aat atc agt ttc gca ttg ccg ggc ggt atg 330
 Ser Phe Met Asp Arg Val Asn Ile Ser Phe Ala Leu Pro Gly Gly Met
 25 30 35
 gag cag gat ctg ctg atg tcc agc cag atg gcc ggg gta gtt agc ggt 378
 Glu Gln Asp Leu Leu Met Ser Ser Gln Met Ala Gly Val Val Ser Gly
 40 45 50 55
 att ttc ttt att ggt tat ctg ttt ttg cag gtt cct ggt ggg cat atc 426
 Ile Phe Phe Ile Gly Tyr Leu Phe Leu Gln Val Pro Gly Gly His Ile
 60 65 70
 gca gta cgt ggc agt ggt aaa cgt ttt att gcc tgg tcg ctt gtt gcc 474
 Ala Val Arg Gly Ser Gly Lys Arg Phe Ile Ala Trp Ser Leu Val Ala

75	80	85	
tgg gcc gtt gtt tct gtc gct acc ggg ttt gtg act cat cag tac cag Trp Ala Val Val Ser Val Ala Thr Gly Phe Val Thr His Gln Tyr Gln 90 95 100			522
ctg ttg att tta cgt ttt gca ctg ggg gtc tct gaa ggt ggg atg ttg Leu Leu Ile Leu Arg Phe Ala Leu Gly Val Ser Glu Gly Gly Met Leu 105 110 115			570
ccg gta gtt ctg aca atg gtc agc aac tgg ttt cct gaa aaa gag ctg Pro Val Val Leu Thr Met Val Ser Asn Trp Phe Pro Glu Lys Glu Leu 120 125 130 135			618
ggg cgt gct aat gca ttt gtc atg atg ttc gcc ccg ctt ggc gga atg Gly Arg Ala Asn Ala Phe Val Met Met Phe Ala Pro Leu Gly Gly Met 140 145 150			666
att acc gcc cct gtc tcc gga tgg att att gca ctg cta gac tgg cgc Ile Thr Ala Pro Val Ser Gly Trp Ile Ile Ala Leu Leu Asp Trp Arg 155 160 165			714
tgg tta ttt att atc gaa gga tta ctg tgc gta gtg gtt ctg gca gtc Trp Leu Phe Ile Ile Glu Gly Leu Leu Ser Val Val Val Leu Ala Val 170 175 180			762
tgg tgg ctg atg gtc agt gac cgc cct gaa gat gcc cgt tgg ctg ccg Trp Trp Leu Met Val Ser Asp Arg Pro Glu Asp Ala Arg Trp Leu Pro 185 190 195			810
gca gca gaa cgg gaa tat ctg ctg cgc gaa atg gcc cgt gac aag gcc Ala Ala Glu Arg Glu Tyr Leu Leu Arg Glu Met Ala Arg Asp Lys Ala 200 205 210 215			858
gag cgg agc aaa ctc cct ccg atc agt cat gct ccc ctg caa gag gtt Glu Arg Ser Lys Leu Pro Pro Ile Ser His Ala Pro Leu Gln Glu Val 220 225 230			906
ttc cat aac ccg ggc ctg atg aag tta gtg att ctg aac ttt ttc tat Phe His Asn Pro Gly Leu Met Lys Leu Val Ile Leu Asn Phe Phe Tyr 235 240 245			954
cag aca ggt gat tac gga tac act ctg tgg ctg ccg act att atc aaa Gln Thr Gly Asp Tyr Gly Tyr Thr Leu Trp Leu Pro Thr Ile Ile Lys 250 255 260			1002
aac ctg acc gga gct agt att ggt aac gtc ggt ttg ctg aca gtg cta Asn Leu Thr Gly Ala Ser Ile Gly Asn Val Gly Leu Leu Thr Val Leu 265 270 275			1050
cct ttt atc gcg acg tta tca ggg att tat gtc gtc tct tac ctg agc Pro Phe Ile Ala Thr Leu Ser Gly Ile Tyr Val Val Ser Tyr Leu Ser 280 285 290 295			1098
gat aaa acc ggc aaa cgt cgg caa tgg gtg atg att tct ctg ttc tgt Asp Lys Thr Gly Lys Arg Arg Gln Trp Val Met Ile Ser Leu Phe Cys 300 305 310			1146

ttt gcg gcc tgc ctg ttg gcc tca gtc ctg tta cgt gaa ttt gtg ctg	1194
Phe Ala Ala Cys Leu Leu Ala Ser Val Leu Leu Arg Glu Phe Val Leu	
315 320 325	
gct gct tat ctg gct ctg gtg gct tgc ggc ttt ttc ctg aaa gca gcc	1242
Ala Ala Tyr Leu Ala Leu Val Ala Cys Gly Phe Phe Leu Lys Ala Ala	
330 335 340	
acc agc ccg ttc tgg agt att ccg gga cgt att gca ccg ccg gaa gca	1290
Thr Ser Pro Phe Trp Ser Ile Pro Gly Arg Ile Ala Pro Pro Glu Ala	
345 350 355	
gcc ggt agt gcc cgt ggt gta att aac gga ctg ggg aat ctg ggc ggt	1338
Ala Gly Ser Ala Arg Gly Val Ile Asn Gly Leu Gly Asn Leu Gly Gly	
360 365 370 375	
ttc tgc ggc ccc tgg ctg gtc gga tta atg atc tac ctg tac gga cag	1386
Phe Cys Gly Pro Trp Leu Val Gly Leu Met Ile Tyr Leu Tyr Gly Gln	
380 385 390	
aat gca gcc gtt gtt act ctg gca ggc tct ctg atc att gcc ggg att	1434
Asn Ala Ala Val Val Thr Leu Ala Gly Ser Leu Ile Ile Ala Gly Ile	
395 400 405	
att gcg gca tta ctg cca acg cag tgt gat ctg cgc ccg gca gag gca	1482
Ile Ala Ala Leu Leu Pro Thr Gln Cys Asp Leu Arg Pro Ala Glu Ala	
410 415 420	
cgg cag cag aat ttc acc cca cgt att cat gat gcc aaa taatactgtc	1531
Arg Gln Gln Asn Phe Thr Pro Arg Ile His Asp Ala Lys	
425 430 435	
accggtaac gctgttgccg ggtgcagcct tcacctttca gggcgtattt ttctgataac	1591
cccgtgtaa	1600

<210> 8

<211> 436

<212> PRT

<213> Pantoea citrea

<400> 8

Met Gln Lys Ser Gln Pro Gly Thr Arg Trp Phe Arg Ile Ile Val Pro	
1 5 10 15	
Ile Leu Ile Ala Cys Ile Met Ser Phe Met Asp Arg Val Asn Ile Ser	
20 25 30	
Phe Ala Leu Pro Gly Gly Met Glu Gln Asp Leu Leu Met Ser Ser Gln	
35 40 45	
Met Ala Gly Val Val Ser Gly Ile Phe Phe Ile Gly Tyr Leu Phe Leu	
50 55 60	
Gln Val Pro Gly Gly His Ile Ala Val Arg Gly Ser Gly Lys Arg Phe	
65 70 75 80	
Ile Ala Trp Ser Leu Val Ala Trp Ala Val Val Ser Val Ala Thr Gly	
85 90 95	
Phe Val Thr His Gln Tyr Gln Leu Leu Ile Leu Arg Phe Ala Leu Gly	
100 105 110	
Val Ser Glu Gly Gly Met Leu Pro Val Val Leu Thr Met Val Ser Asn	

115	120	125
Trp Phe Pro Glu Lys Glu Leu Gly Arg Ala Asn Ala Phe Val Met Met		
130	135	140
Phe Ala Pro Leu Gly Gly Met Ile Thr Ala Pro Val Ser Gly Trp Ile		
145	150	155
Ile Ala Leu Leu Asp Trp Arg Trp Leu Phe Ile Ile Glu Gly Leu Leu		
165	170	175
Ser Val Val Val Leu Ala Val Trp Trp Leu Met Val Ser Asp Arg Pro		
180	185	190
Glu Asp Ala Arg Trp Leu Pro Ala Ala Glu Arg Glu Tyr Leu Leu Arg		
195	200	205
Glu Met Ala Arg Asp Lys Ala Glu Arg Ser Lys Leu Pro Pro Ile Ser		
210	215	220
His Ala Pro Leu Gln Glu Val Phe His Asn Pro Gly Leu Met Lys Leu		
225	230	235
Val Ile Leu Asn Phe Phe Tyr Gln Thr Gly Asp Tyr Gly Tyr Thr Leu		
245	250	255
Trp Leu Pro Thr Ile Ile Lys Asn Leu Thr Gly Ala Ser Ile Gly Asn		
260	265	270
Val Gly Leu Leu Thr Val Leu Pro Phe Ile Ala Thr Leu Ser Gly Ile		
275	280	285
Tyr Val Val Ser Tyr Leu Ser Asp Lys Thr Gly Lys Arg Arg Gln Trp		
290	295	300
Val Met Ile Ser Leu Phe Cys Phe Ala Ala Cys Leu Leu Ala Ser Val		
305	310	315
Leu Leu Arg Glu Phe Val Leu Ala Ala Tyr Leu Ala Leu Val Ala Cys		
325	330	335
Gly Phe Phe Leu Lys Ala Ala Thr Ser Pro Phe Trp Ser Ile Pro Gly		
340	345	350
Arg Ile Ala Pro Pro Glu Ala Ala Gly Ser Ala Arg Gly Val Ile Asn		
355	360	365
Gly Leu Gly Asn Leu Gly Gly Phe Cys Gly Pro Trp Leu Val Gly Leu		
370	375	380
Met Ile Tyr Leu Tyr Gly Gln Asn Ala Ala Val Val Thr Leu Ala Gly		
385	390	395
Ser Leu Ile Ile Ala Gly Ile Ile Ala Ala Leu Leu Pro Thr Gln Cys		
405	410	415
Asp Leu Arg Pro Ala Glu Ala Arg Gln Gln Asn Phe Thr Pro Arg Ile		
420	425	430
His Asp Ala Lys		
435		

<210> 9
 <211> 1500
 <212> DNA
 <213> Pantoea citrea

<220>
 <221> CDS
 <222> (154)...(1440)

<400> 9	
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gcctcagtat aaaatacagg ggcagacgga atcagagttt gccctgaaga tatcttactg	120
gttgcccctt cggcacacac aggatgttcc ccc atg aat aca agc aga aaa ctg	174
Met Asn Thr Ser Arg Lys Leu	
1 5	

ccg gtg aaa cgc tgg tgg tat tta atg ccg gtg att ttt att act tac	222
Pro Val Lys Arg Trp Trp Tyr Leu Met Pro Val Ile Phe Ile Thr Tyr	
10 15 20	
agc ctg gca tat ctg gat cgg gcc aac tac ggc ttt gct gct gcc tct	270
Ser Leu Ala Tyr Leu Asp Arg Ala Asn Tyr Gly Phe Ala Ala Ala Ser	
25 30 35	
ggg att gaa gca gat ctt gga att agc cgt ggc acc tcc tct ctg att	318
Gly Ile Glu Ala Asp Leu Gly Ile Ser Arg Gly Thr Ser Ser Leu Ile	
40 45 50 55	
gga gca ctg ttc ttt ctc ggc tac ttc att ttt cag gtg ccc ggg gca	366
Gly Ala Leu Phe Phe Leu Gly Tyr Phe Ile Phe Gln Val Pro Gly Ala	
60 65 70	
att tat gca gtg aaa cgc agt gtc cgt aaa ctg gtg ttt acc agc ctg	414
Ile Tyr Ala Val Lys Arg Ser Val Arg Lys Leu Val Phe Thr Ser Leu	
75 80 85	
ctg ttg tgg gga ttt tgt gcc gct gcg acc gga ctt atc agc aat att	462
Leu Leu Trp Gly Phe Cys Ala Ala Thr Gly Leu Ile Ser Asn Ile	
90 95 100	
ccg gct ctg atg gtg atc cgc ttt gtt ctg ggt gtt gtt gaa gcc gca	510
Pro Ala Leu Met Val Ile Arg Phe Val Leu Gly Val Val Glu Ala Ala	
105 110 115	
gtg atg cca gcg atg ctg att tac atc agc aac tgg ttc acc cgt cag	558
Val Met Pro Ala Met Leu Ile Tyr Ile Ser Asn Trp Phe Thr Arg Gln	
120 125 130 135	
gaa cgt tca cgg gct aat acc ttt ctg gta tta ggt aac ccg gtc acg	606
Glu Arg Ser Arg Ala Asn Thr Phe Leu Val Leu Gly Asn Pro Val Thr	
140 145 150	
gtg tta tgg atg tct att gtt tcc gga tat ctg atc aat gct ttt ggc	654
Val Leu Trp Met Ser Ile Val Ser Gly Tyr Leu Ile Asn Ala Phe Gly	
155 160 165	
tgg cgg gaa atg ttt att ttc gag ggt gtg cct gcc tta atc tgg gcc	702
Trp Arg Glu Met Phe Ile Phe Glu Gly Val Pro Ala Leu Ile Trp Ala	
170 175 180	
atc ttc tgg tgg ttt att gtc cgg gac aaa ccg gag cag gtg agc tgg	750
Ile Phe Trp Trp Phe Ile Val Arg Asp Lys Pro Glu Gln Val Ser Trp	
185 190 195	
ctg aca gaa aca gaa aag cag caa ctg gcc agt gca atg gct gaa gag	798
Leu Thr Glu Thr Glu Lys Gln Gln Leu Ala Ser Ala Met Ala Glu Glu	
200 205 210 215	
cag cag gca ata cca ccg atg cgc aat gtg ccg cag gcc ctg cgt tcc	846
Gln Gln Ala Ile Pro Pro Met Arg Asn Val Pro Gln Ala Leu Arg Ser	
220 225 230	

cgc aat gtg gtg gta ctg tgc ctg tta cac gct ctg tgg agc atc gga Arg Asn Val Val Val Leu Cys Leu Leu His Ala Leu Trp Ser Ile Gly 235 240 245	894
gtg tat ggt ttt atg atg tgg atg cca tcg ata ctg cgt agc gct gca Val Tyr Gly Phe Met Met Trp Met Pro Ser Ile Leu Arg Ser Ala Ala 250 255 260	942
tca atg gac att gtc cgg gta ggc tgg ctg gcc gca gtt ccg tat ctg Ser Met Asp Ile Val Arg Val Gly Trp Leu Ala Ala Val Pro Tyr Leu 265 270 275	990
gcc gcg att att act atg ctg gtg att tca tgg ctg tca gat aaa acc Ala Ala Ile Ile Thr Met Leu Val Ile Ser Trp Leu Ser Asp Lys Thr 280 285 290 295	1038
ggg ctg cgt cgg ctt ttt atc tgg cca tta ttg ctg att gcg tca gtt Gly Leu Arg Arg Leu Phe Ile Trp Pro Leu Leu Leu Ile Ala Ser Val 300 305 310	1086
act ttt ttt ggg tcc tgg tta ctt ggg agc tac tca ttc tgg ttt tcc Thr Phe Phe Gly Ser Trp Leu Leu Gly Ser Tyr Ser Phe Trp Phe Ser 315 320 325	1134
tat ggc ttg ctg gta ctg gct gct gct tgt atg tat gcc ccg tat gga Tyr Gly Leu Leu Val Leu Ala Ala Ala Cys Met Tyr Ala Pro Tyr Gly 330 335 340	1182
ccg ttt ttt gcg ttg att cct gaa ttg ctg cca aaa aat gtg gcg ggg Pro Phe Phe Ala Leu Ile Pro Glu Leu Leu Pro Lys Asn Val Ala Gly 345 350 355	1230
att tct atc ggg tta att aac tgt tgc ggg gcg ctg gga gct ttt gcc Ile Ser Ile Gly Leu Ile Asn Cys Cys Gly Ala Leu Gly Ala Phe Ala 360 365 370 375	1278
gga gcc tgg ctg gtg ggc tat ctt aat ggt ctg acc ggt ggt ccg ggg Gly Ala Trp Leu Val Gly Tyr Leu Asn Gly Leu Thr Gly Gly Pro Gly 380 385 390	1326
gct tct tac act ttt atg gcc att gca ttg ctg gtt tct gta ggg ttg Ala Ser Tyr Thr Phe Met Ala Ile Ala Leu Leu Val Ser Val Gly Leu 395 400 405	1374
gtg ttt ttc ctg aaa gtc cct tca ggg aat ttg gtc act cgt cgg ttg Val Phe Phe Leu Lys Val Pro Ser Gly Asn Leu Val Thr Arg Arg Leu 410 415 420	1422
ctg aaa ggt gat gca aag taaaaggaat agcgatgaaa cggaacagga Leu Lys Gly Asp Ala Lys 425	1470
tgtcttttgca ggatattgcg gacctcgccg	1500
<210> 10	
<211> 429	
<212> PRT	

<213> Pantoea citrea

<400> 10

Met	Asn	Thr	Ser	Arg	Lys	Leu	Pro	Val	Lys	Arg	Trp	Trp	Tyr	Leu	Met
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Pro	Val	Ile	Phe	Ile	Thr	Tyr	Ser	Leu	Ala	Tyr	Leu	Asp	Arg	Ala	Asn
		20						25				30			
Tyr	Gly	Phe	Ala	Ala	Ala	Ser	Gly	Ile	Glu	Ala	Asp	Leu	Gly	Ile	Ser
	35						40				45				
Arg	Gly	Thr	Ser	Ser	Leu	Ile	Gly	Ala	Leu	Phe	Phe	Leu	Gly	Tyr	Phe
	50				55					60					
Ile	Phe	Gln	Val	Pro	Gly	Ala	Ile	Tyr	Ala	Val	Lys	Arg	Ser	Val	Arg
65					70				75					80	
Lys	Leu	Val	Phe	Thr	Ser	Leu	Leu	Leu	Trp	Gly	Phe	Cys	Ala	Ala	Ala
			85						90					95	
Thr	Gly	Leu	Ile	Ser	Asn	Ile	Pro	Ala	Leu	Met	Val	Ile	Arg	Phe	Val
		100						105					110		
Leu	Gly	Val	Val	Glu	Ala	Ala	Val	Met	Pro	Ala	Met	Leu	Ile	Tyr	Ile
	115						120					125			
Ser	Asn	Trp	Phe	Thr	Arg	Gln	Glu	Arg	Ser	Arg	Ala	Asn	Thr	Phe	Leu
	130					135					140				
Val	Leu	Gly	Asn	Pro	Val	Thr	Val	Leu	Trp	Met	Ser	Ile	Val	Ser	Gly
145					150					155					160
Tyr	Leu	Ile	Asn	Ala	Phe	Gly	Trp	Arg	Glu	Met	Phe	Ile	Phe	Glu	Gly
			165					170						175	
Val	Pro	Ala	Leu	Ile	Trp	Ala	Ile	Phe	Trp	Trp	Phe	Ile	Val	Arg	Asp
		180						185					190		
Lys	Pro	Glu	Gln	Val	Ser	Trp	Leu	Thr	Glu	Thr	Glu	Lys	Gln	Gln	Leu
	195						200					205			
Ala	Ser	Ala	Met	Ala	Glu	Glu	Gln	Gln	Ala	Ile	Pro	Pro	Met	Arg	Asn
	210					215					220				
Val	Pro	Gln	Ala	Leu	Arg	Ser	Arg	Asn	Val	Val	Val	Leu	Cys	Leu	Leu
225					230					235					240
His	Ala	Leu	Trp	Ser	Ile	Gly	Val	Tyr	Gly	Phe	Met	Met	Trp	Met	Pro
			245						250					255	
Ser	Ile	Leu	Arg	Ser	Ala	Ala	Ser	Met	Asp	Ile	Val	Arg	Val	Gly	Trp
		260						265					270		
Leu	Ala	Ala	Val	Pro	Tyr	Leu	Ala	Ala	Ile	Ile	Thr	Met	Leu	Val	Ile
	275						280					285			
Ser	Trp	Leu	Ser	Asp	Lys	Thr	Gly	Leu	Arg	Arg	Leu	Phe	Ile	Trp	Pro
	290					295					300				
Leu	Leu	Leu	Ile	Ala	Ser	Val	Thr	Phe	Phe	Gly	Ser	Trp	Leu	Leu	Gly
305					310					315					320
Ser	Tyr	Ser	Phe	Trp	Phe	Ser	Tyr	Gly	Leu	Leu	Val	Leu	Ala	Ala	Ala
			325						330					335	
Cys	Met	Tyr	Ala	Pro	Tyr	Gly	Pro	Phe	Phe	Ala	Leu	Ile	Pro	Glu	Leu
		340						345					350		
Leu	Pro	Lys	Asn	Val	Ala	Gly	Ile	Ser	Ile	Gly	Leu	Ile	Asn	Cys	Cys
	355						360					365			
Gly	Ala	Leu	Gly	Ala	Phe	Ala	Gly	Ala	Trp	Leu	Val	Gly	Tyr	Leu	Asn
	370					375					380				
Gly	Leu	Thr	Gly	Gly	Pro	Gly	Ala	Ser	Tyr	Thr	Phe	Met	Ala	Ile	Ala
385					390					395					400
Leu	Leu	Val	Ser	Val	Gly	Leu	Val	Phe	Phe	Leu	Lys	Val	Pro	Ser	Gly
			405						410					415	
Asn	Leu	Val	Thr	Arg	Arg	Leu	Leu	Lys	Gly	Asp	Ala	Lys			
			420						425						

<210> 11
 <211> 1500
 <212> DNA
 <213> Klebsiella oxytoca

<220>
 <221> CDS
 <222> (70)...(1386)

<400> 11
 ctaaaacaag cacaataata ataatcacct tcatcaccag aatattttta atattacgag 60
 actataaag atg aat ata acc tct aac tct aca acc aaa gat ata ccg cgc 111
 Met Asn Ile Thr Ser Asn Ser Thr Thr Lys Asp Ile Pro Arg
 1 5 10

cag cgc tgg tta aga atc att ccg cct ata ctg atc act tgt att att 159
 Gln Arg Trp Leu Arg Ile Ile Pro Pro Ile Leu Ile Thr Cys Ile Ile
 15 20 25 30

tct tat atg gac cgg gtc aat att gcc ttt gcg atg ccc gga ggt atg 207
 Ser Tyr Met Asp Arg Val Asn Ile Ala Phe Ala Met Pro Gly Gly Met
 35 40 45

gat gcc gac tta ggt att tcc gcc acc atg gcg ggg ctg gcg ggc ggt 255
 Asp Ala Asp Leu Gly Ile Ser Ala Thr Met Ala Gly Leu Ala Gly Gly
 50 55 60

att ttc ttt atc ggt tat cta ttt tta cag gtt ccc ggc ggg aaa att 303
 Ile Phe Phe Ile Gly Tyr Leu Phe Leu Gln Val Pro Gly Gly Lys Ile
 65 70 75

gcc gtt cac ggt agc ggt aag aaa ttt atc ggc tgg tcg ctg gtc gcc 351
 Ala Val His Gly Ser Gly Lys Lys Phe Ile Gly Trp Ser Leu Val Ala
 80 85 90

tgg gcg gtc atc tcc gtg ctg acg ggg tta att acc aat cag tac cag 399
 Trp Ala Val Ile Ser Val Leu Thr Gly Leu Ile Thr Asn Gln Tyr Gln
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 Leu Leu Ala Leu Arg Phe Leu Leu Gly Val Ala Glu Gly Gly Met Leu
 115 120 125

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 Pro Val Val Leu Thr Met Ile Ser Asn Trp Phe Pro Asp Ala Glu Arg
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atc acc gcc cca ctc tca ggc tgg att atc acg gtt ctc gac tgg cgc 591
 Ile Thr Ala Pro Leu Ser Gly Trp Ile Ile Thr Val Leu Asp Trp Arg
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Trp	Ala	Tyr	Thr	Ile	Tyr	Asp	Arg	Pro	Gln	Glu	Ala	Arg	Trp	Ile	Ser		
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Glu	Ala	Glu	Lys	Arg	Tyr	Leu	Val	Glu	Thr	Leu	Ala	Ala	Glu	Gln	Lys		
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Ala	Ile	Ala	Gly	Thr	Glu	Val	Lys	Asn	Ala	Ser	Leu	Ser	Ala	Val	Leu		
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Ser	Asp	Lys	Thr	Met	Trp	Gln	Leu	Ile	Ala	Leu	Asn	Phe	Phe	Tyr	Gln		
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Thr	Gly	Ile	Tyr	Gly	Tyr	Thr	Leu	Trp	Leu	Pro	Thr	Ile	Leu	Lys	Glu		
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Tyr	Val	Gly	Ala	Ile	Ala	Gly	Met	Phe	Leu	Phe	Ser	Ser	Leu	Ser	Asp		
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Ser	Tyr	Ala	Ala	Leu	Val	Gly	Cys	Gly	Phe	Phe	Leu	Gln	Ser	Ala	Ala		
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Gly	Val	Phe	Trp	Thr	Ile	Pro	Ala	Arg	Leu	Phe	Ser	Ala	Glu	Met	Ala		
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Gly	Gly	Ala	Arg	Gly	Val	Ile	Asn	Ala	Leu	Gly	Asn	Leu	Gly	Gly	Phe		
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Cys	Gly	Pro	Tyr	Ala	Val	Gly	Val	Leu	Ile	Thr	Leu	Tyr	Ser	Lys	Asp		
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Thr Ile Asn Pro His Lys Arg Thr Ala			
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Phe Ile Ile Glu Gly Leu Leu Ser Leu Val Val Leu Val Leu Trp Ala			
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Tyr Thr Ile Tyr Asp Arg Pro Gln Glu Ala Arg Trp Ile Ser Glu Ala			
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Glu Lys Arg Tyr Leu Val Glu Thr Leu Ala Ala Glu Gln Lys Ala Ile			
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Lys Thr Met Trp Gln Leu Ile Ala Leu Asn Phe Phe Tyr Gln Thr Gly			
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Gly Ala Ile Ala Gly Met Phe Leu Phe Ser Ser Leu Ser Asp Arg Thr			
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 Cys Met Phe Leu Ser Val Ala Leu Lys Asn Gln Ile Trp Leu Ser Tyr
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 Ala Arg Gly Val Ile Asn Ala Leu Gly Asn Leu Gly Gly Phe Cys Gly
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 Pro Tyr Ala Val Gly Val Leu Ile Thr Leu Tyr Ser Lys Asp Ala Gly
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 Val Tyr Cys Leu Ala Ile Ser Leu Ala Leu Ala Ala Leu Met Ala Leu
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 Met Ser
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 Lys Ile Asp Val Leu Gln Val Gly Pro Tyr Pro Ala Trp Asp Glu Glu
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 Arg Leu Asn Ala Thr Phe Thr Met His Arg Tyr Phe Glu Ala Ala Asp
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 Lys Ala Ala Phe Leu Ala Glu His Gly Gly Thr Ile Arg Gly Ile Ala
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 Thr Arg Gly Glu Leu Gly Ala Asn Arg Ala Met Ile Glu Ala Leu Pro

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Leu	Ser	Ala	Ala	Arg	Glu	Arg	Gly	Ile	Arg	Val	Thr	Asn	Thr	Pro	Asp					
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Lys	Asp	Phe	Ala	Arg	Asp	Trp	Thr	Phe	Val	Ala	Asp	Pro	Ala	Glu	Leu					
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Thr	Arg	His	Ile	Val	Gly	Arg	Lys	Val	Ile	Glu	Ala	Leu	Gly	Pro	Glu					
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Pro Tyr Thr Ala Thr Lys Gly Ala Val Gly Asn Leu Thr Lys Gly Met	
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Phe Ser Ala Trp Leu Glu Lys Arg Thr Pro Ala Gly Arg Trp Gly Lys	
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Leu	Asp	Val	Phe	Glu	Gly	Glu	Pro	Asn	Leu	Asn	Pro	Arg	Phe	Leu	Ala
		260						265					270		
Leu	Asp	Asn	Val	Leu	Leu	Gln	Pro	His	Met	Ala	Ser	Gly	Thr	Ile	Glu
		275					280					285			
Thr	Arg	Lys	Ala	Met	Gly	Gln	Leu	Val	Phe	Asp	Asn	Leu	Ser	Ala	His
	290					295					300				
Phe	Asp	Gly	Arg	Pro	Leu	Pro	Thr	Pro	Val	Leu					
305					310					315					

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<211> 343

<212> PRT

<213> environmental source

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Met	Lys	Ala	Ile	Val	Ile	His	Gln	Ala	Lys	Asp	Leu	Arg	Val	Glu	Asp
1			5						10					15	
Ser	Ala	Val	Glu	Ala	Pro	Gly	Pro	Gly	Glu	Val	Glu	Ile	Arg	Leu	Ala
		20						25					30		
Ala	Gly	Gly	Ile	Cys	Gly	Ser	Asp	Leu	His	Tyr	Tyr	Asn	His	Gly	Gly
		35					40					45			
Phe	Gly	Thr	Val	Arg	Leu	Lys	Glu	Pro	Met	Ile	Leu	Gly	His	Glu	Val
	50					55					60				
Ser	Gly	His	Val	Ala	Ala	Leu	Gly	Glu	Gly	Val	Ser	Gly	Leu	Ala	Ile
65					70				75					80	
Gly	Asp	Leu	Val	Ala	Val	Ser	Pro	Ser	Arg	Pro	Cys	Gly	Ala	Cys	Asp
				85					90					95	

Tyr Cys Leu Lys Gly Leu Ala Asn His Cys Phe Asn Met Arg Phe Tyr
 100 105 110
 Gly Ser Ala Met Pro Phe Pro His Ile Gln Gly Ala Phe Arg Glu Arg
 115 120 125
 Leu Val Ala Lys Ala Ser Gln Cys Val Lys Ala Glu Gly Leu Ser Ala
 130 135 140
 Gly Glu Ala Ala Met Ala Glu Pro Leu Ser Val Thr Leu His Ala Thr
 145 150 155 160
 Arg Arg Ala Gly Glu Met Leu Gly Lys Arg Val Leu Val Thr Gly Cys
 165 170 175
 Gly Pro Ile Gly Thr Leu Ser Ile Leu Ala Ala Arg Arg Ala Gly Ala
 180 185 190
 Ala Glu Ile Val Ala Ala Asp Leu Ser Glu Arg Ala Leu Gly Phe Ala
 195 200 205
 Arg Ala Val Gly Ala Asp Arg Thr Val Asn Leu Ser Glu Asp Arg Asp
 210 215 220
 Gly Leu Val Pro Phe Ser Glu Asn Lys Gly Tyr Phe Asp Val Leu Tyr
 225 230 235 240
 Glu Cys Ser Gly Ala Gln Pro Ala Leu Val Ala Gly Ile Gln Ala Leu
 245 250 255
 Arg Pro Arg Gly Val Ile Val Gln Leu Gly Leu Gly Glu Met Ser
 260 265 270
 Leu Pro Met Met Ala Ile Thr Ala Lys Glu Leu Asp Leu Arg Gly Ser
 275 280 285
 Phe Arg Phe His Glu Glu Phe Ala Val Ala Val Lys Leu Met Gln Gly
 290 295 300
 Gly Leu Ile Asp Val Lys Pro Leu Ile Thr His Thr Leu Pro Leu Ala
 305 310 315 320
 Asp Ala Leu Gln Ala Phe Glu Ile Ala Ser Asp Lys Gly Gln Ser Met
 325 330 335
 Lys Thr Gln Ile Ala Phe Ser
 340

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<211> 251

<212> PRT

<213> environmental source

<400> 16

Met Ser Ile Gln Leu Phe Asp Leu Thr Gly Lys Arg Ala Leu Val Thr
 1 5 10 15
 Gly Ser Ser Gln Gly Ile Gly Tyr Ala Leu Ala Lys Gly Leu Ala Ala
 20 25 30
 Ala Gly Ala Asp Ile Val Leu Asn Gly Arg Asp Ala Ala Lys Leu Ala
 35 40 45
 Ala Ala Ala Gln Glu Leu Gly Ala Lys His Thr Leu Ala Phe Asp Ala
 50 55 60
 Thr Asp His Ala Ala Val Arg Ala Ala Ile Asp Ala Phe Glu Ala Glu
 65 70 75 80
 Val Gly Pro Ile Asp Ile Leu Val Asn Asn Ala Gly Met Gln His Arg
 85 90 95
 Thr Pro Leu Glu Asp Phe Pro Ala Asp Ala Phe Glu Arg Ile Leu Lys
 100 105 110
 Thr Asn Ile Ser Thr Val Phe Asn Val Gly Gln Ala Val Ala Arg His
 115 120 125
 Met Ile Ala Arg Gly Ala Gly Lys Ile Ile Asn Ile Ala Ser Val Gln
 130 135 140

Thr	Ala	Leu	Ala	Arg	Pro	Gly	Ile	Ala	Pro	Tyr	Thr	Ala	Thr	Lys	Gly
145					150					155					160
Ala	Val	Gly	Asn	Leu	Thr	Lys	Gly	Met	Ala	Thr	Asp	Trp	Ala	Lys	Tyr
			165						170					175	
Gly	Leu	Gln	Cys	Asn	Ala	Ile	Ala	Pro	Gly	Tyr	Phe	Asp	Thr	Pro	Leu
		180						185					190		
Asn	Ala	Ala	Leu	Val	Ala	Asp	Pro	Ala	Phe	Ser	Ala	Trp	Leu	Glu	Lys
	195						200					205			
Arg	Thr	Pro	Ala	Gly	Arg	Trp	Gly	Lys	Val	Glu	Glu	Leu	Ile	Gly	Ala
	210					215					220				
Cys	Ile	Phe	Leu	Ser	Ser	Asp	Ala	Ser	Ser	Phe	Val	Asn	Gly	His	Thr
225					230					235					240
Leu	Tyr	Val	Asp	Gly	Gly	Ile	Thr	Ala	Ser	Leu					
				245					250						

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 <212> DNA
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<220>
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32

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 <212> DNA
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<400> 18
 cgtatctaga aaaatattct ggtgatgaag gtga

34

<210> 19
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 <212> DNA
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<220>
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<400> 19
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34

<210> 20
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 <212> DNA
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<220>
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<400> 20

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33

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<212> DNA

<213> Artificial Sequence

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<400> 21

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31

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<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 22

cataggtacc ggcttttcaga taggtgcc

28